

SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd

5

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTANOATE

<130>

10

<140>

<141>

<160> 27

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<170> PatentIn Ver. 2.1

<210> 1

<211> 325

20

<212> PRT

<213> Penicillium citrinum

<400> 1

Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro

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Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
20 25 30

30

Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
35 40 45Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
50 55 60

35

Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
65 70 75 80

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Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
85 90 95

Lys Asn Leu Ser Ala
325

5 <210> 2
 <211> 978
 <212> DNA
 <213> Penicillium citrinum

10 <220>
 <221> CDS
 <222> (1).. (978)

<400> 2

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15 ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc
 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
 20 25 30

20 tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac
 Tyr Thr Ala Val Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
 25 35 40 45

25 tgg gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt
 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
 50 55 60

30 gac ttc ctg aag gag aac ccc tgg gtg aag cgt gag gac atc ttc gtc
 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
 65 70 75 80

35 tgg acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg
 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
 85 90 95

40 tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg
 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110

336

Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110

Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 5 115 120 125

Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140

10 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160

Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175

15 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190

Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 195 200 205

Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220

25 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240

Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255

30 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270

Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 35 275 280 285

Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 290 295 300

40 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
 305 310 315 320

ttc ctc gti cac tgg ccc att gct gcc gag aag aat gcc cag ggt gag
 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125 384

5 ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140 432

10 gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160 480

15 cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175 528

20 gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190 576

25 gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 195 200 205 624

30 tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220 672

35 cag gtt ccc acc acc ggt gag ogg gtc agc gag aac aag act ctg aac
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240 720

gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255 768

40 tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270 816

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 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 864

275 280 285

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 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 5 290 295 300

aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc 960
 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
 305 310 315 320

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aag aac ctg tct gcg tga 978
 Lys Asn Leu Ser Ala
 325

15

<210> 3
 <211> 17
 <212> PRT
 <213> Penicillium citrinum

20

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Pro

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<210> 4
 <211> 10
 <212> PRT
 <213> Penicillium citrinum

35

<400> 4
 Ile Pro Gly Val Phe Gly Thr Phe Ala Ser
 1 5 10

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<210> 5
 <211> 17
 <212> PRT
 <213> Penicillium citrinum

<400> 5

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1 5 10 15

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Lys

10 <210> 6

<211> 14

<212> PRT

<213> Penicillium citrinum

15 <400> 6

Met Ile Gly Val Ala Asn Tyr Thr Ile Ala Asp Leu Glu Lys
1 5 10

20 <210> 7

<211> 14

<212> PRT

<213> Penicillium citrinum

25 <400> 7

Tyr Glu Asp Val Leu Xaa Xaa Ile Asp Asp Ser Leu Lys Arg
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30 <210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

35 <220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

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<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

5 <220>
<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

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tangcnacng gcataatatt 20

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<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 10
tangcnacng gcataatgtt 20

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

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tangcnacng gcatgatatt 20

<210> 12
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
5 oligonucleotide primer for PCR

<400> 12

tangcnacng gcatgatgtt

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<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

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<400> 13

tangcnacng gcattatatt

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<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

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<220>

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<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

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<400> 14

tangcnacng gcattatgtt

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35

<210> 15

<211> 697

<212> DNA

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<213> Escherichia coli

<400> 15

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 agtgaagggtt ccaaggcgaa aacctatnct gctgtcacca ctgcctgaa aaccggttac 180
 cgtcncttgg actgtgcctg gtactacctg aacaagggtg agttggta gggtnccgt 240
 5 gacttcctga aggaaaaccc ctcggtaag cgtgaggaca tottoltc caccaggta 300
 tggaaaccacc tccaccgtta tgaggacgtc ctctggtcca ttgacnactc cctgaagggt 360
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 gaaaanccna nccccctgg cgogctatgg aaaaaatttn tgangatccc aaggccaggt 540
 10 ccattggtgt ttccaaattgg accattggcg acottgagaa gatgtccaag ttncccaagg 600
 tnatgcctca cgccaaaccag atcgagatc accccttctt gcccaacgag gagctggtgc 660
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15 <210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

20 <220>

<223> Description of Artificial Sequence: Designed
oligonucleotide primer for PCR

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ggaggtggtt ccacacottg g

21

30 <210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

35 <220>

<223> Description of Artificial Sequence: Designed
oligonucleotide primer for PCR

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caaccagatc gagattcacc

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<210> 18

<211> 331

<212> DNA

<213> Escherichia coli

<400> 18

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ggcttggta ctttcgttag tgaagggtcc aaggggcgaga cctatactgc tgtcaccaact 180
gcocctgaaga ccgggttaccg tcacttggac tgtgcctggactaacctgaa cgagggtgag 240
gttggtgagg gtatccgtga cttcttgaag gagaaccctt cggtaagcgc tgaggacatc 300
10 ttcgtctgca ccaagggtgtc gaaccacatc 331

<210> 19

<211> 743

<212> DNA

<213> *Escherichia coli*

<400> 19

<210> 20

35 <211> 21

<212> DNA

<213> Artificial Sequence

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40 <223> Description of Artificial Sequence:Designed
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<400> 20

ccaagggtgtg gaaccacac c

21

5 <210> 21

<211> 21

<212> DNA

<213> Artificial Sequence

10 <220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

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ccaaaggaggaga gtagggccacg g

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20 <210> 22

<211> 417

<212> DNA

<213> Escherichia coli

25 <400> 22

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agaagaatgg ccagggtgag cccaaaggattt gcccgtacgg caaaatacgcc attctcaagg 180

acctgacccga gaaccccgag cccacatggc gcgctatggta gaagatttat gaggatcgca 240

aggccaggtc cattgggtgc tccaaactggta ccattggcga ctttggaaaat atgtccaaat 300

tcggccaaaggat catgcctcac gccaaccaga tcggatccaa ccccttccgt cccaaacggagg 360

30 agctggtgca gtactgtttc tccaaagaaca ttatggccgt ggccctactctt cctctgg 417

35 <210> 23

<211> 27

<212> DNA

<213> Artificial Sequence

40 <220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

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gccatggcta tgtctaacgg aaagact

27

<210> 24

5 <211> 29

<212> DNA

<213> Artificial Sequence

<220>

10 <223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 24

15 cgatatccgtt ataatttgcgt agagattca

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<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

20 <223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 25

25 gatcatcata gcaggagtca t

21

30 <210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

35 <220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 26

40 gaattcaaca ccagttagct c

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<210> 27
<211> 786
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS
<222> (1)...(786)

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1 5 10 15

15 acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct 96
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
20 25 30

aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gaa gct aac agc gtt 144
 Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
 35 40 45

192

tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ala Ile Ala Val Lys Gly	50	55	60
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gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att	240
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile	
65 70 75 80	

aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa 288
 Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
 85 90 95

35 aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc 336
 Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
 100 105 110

40 att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att 384
 Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125

PROTEIN SEQUENCE

	aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg	432
	Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser	
	130 135 140	
5	agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca	480
	Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
	145 150 155 160	
10	agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac	528
	Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
	165 170 175	
15	gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat	576
	Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
	180 185 190	
20	aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat	624
	Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp	
	195 200 205	
25	gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att	672
	Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
	210 215 220	
30	gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca	720
	Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr	
	225 230 235 240	
35	ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc	768
	Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	
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	Gln Ala Gly Arg Gly	
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	<211> 996	
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	<213> Penicillium citrinum	

<220>

<221> CDS

<222> (1).. (978)

5 <400> 28

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10 ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc
 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
 20 25 30

15 tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac
 Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
 35 40 45

20 tgg gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt
 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Ile Arg
 50 55 60

25 gac ttc ctg aag gag aac ccc tcc gtg aag cgt gag gac atc ttc gtc
 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
 65 70 75 80

30 tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg
 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
 85 90 95

35 tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg
 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110

40 ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag
 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125

45 ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140

50 gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat 480

	Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp			
145	150	155	160	
5	cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	165	170	175
10	gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	180	185	190
15	gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	195	200	205
20	tcc aag aac att atg ccc gtg gco tac tct cct ctg ggc tcg cag aac Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	210	215	220
25	cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	225	230	235
30	240			
35	gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala	245	250	255
40	tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro	260	265	270
45	285			
50	aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp	275	280	
55	295			
60	ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val	290	300	
65	310			
70	315			
75	320			
80	960			

aag aac ctg tct gcg tga atctctacga aattataaa 996

Lys Asn Leu Ser Ala

325

5

<210> 29

<211> 29

<212> DNA

<213> Artificial Sequence

10

<220>

<223> Description of Artificial Sequence Designed oligonucleotide primer
for PCR

15

<400> 29

cggatccgtt cacgcagaca gtttcttgg

29

<210> 30

<211> 978

20

<212> DNA

<213> Penicillium citrinum

25

<220>

<221> GDS

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<222> (1)..(978)

<400> 30

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Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro

35

1

5

10

15

ggc gtc ggc ttt ggt acc ttc got agt gaa ggt tcc aag ggc gag acc 96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
20 25 30

35

tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac 144
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
35 40 45

40

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag egt atc cgt 192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
50 55 60

gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc 240
 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
 65 70 75 80

5 tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg 288
 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
 85 90 95

10 tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg 336
 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110

15 ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag 384
 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125

20 ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc 432
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140

25 gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat 480
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160

30 cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt 528
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175

35 gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc 576
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190

40 gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc 624
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 195 200 205

tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcc cag aac 672
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220

cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac 720

Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240

5 gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc 768
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255

10 tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc 816
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270

15 aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac 864
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 275 280 285

20 ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc 912
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 290 295 300

25 aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc 960
 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
 305 310 315 320

30 aag aac ctg tot gcg tga 978
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30 <212> DNA

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<220>

35 <223> Description of Artificial Sequence Designed oligonucleotide primer
for PCR

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5 <223> Description of Artificial Sequence Designed oligonucleotide primer
for PCR

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23

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for PCR

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<210> 34

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25 <212> PRT

<213> Corynebacterium sp.

<400> 34

Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr

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10

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Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
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35 40 45Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
50 55 60

Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
65 70 75 80

5 Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
85 90 95

His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
100 105 110

Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
115 120 125

Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
130 135 140

Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
145 150 155 160

20 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
180 185 190

25 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
195 200 205

Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
210 215 220

Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
225 230 235 240

35 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
260 265 270

40 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
275 280 285

Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
 290 295 300

5 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp
 305 310 315 320

Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg
 325 330 335

10 Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr
 340 345 350

15 Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile
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Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro
 370 375 380

20 Arg
 385

25 <210> 35

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<213> Corynebacterium sp.

30 <220>
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 1 5 10 15

40 gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc otg gaa gtc 96
 Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
 20 25 30

acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc 144

	Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro		
	35	40	45
5	gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly		192
	50	55	60
10	gca ggc aag gtc gcc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile		240
	65	70	75
	80		
15	gga acc aat gtc gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp		288
	85	90	95
20	cac tgc tca caa gga ctc gag aac tat tgc tot cgc gcc caa gaa ctc His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu		336
	100	105	110
25	gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe		384
	115	120	125
30	atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp		432
	130	135	140
	140		
35	ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His		480
	145	150	155
	160		
40	gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val		528
	165	170	175
	180	185	190
	190		
45	gtc att ggt acc ggc ggt ctc ggc cac gtc got att cag ctc ctc cgc Val Ile Gly Thr Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg		576
	195	200	205
	205		

ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac 672
 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 210 215 220
 5
 aag gac gcg gcc gag aac gtc ogo aag atc act gga agt caa ggo gcc 720
 Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gin Gly Ala
 225 230 235 240
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 gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg 768
 Ala Leu Val Leu Asp Phe Val Gly Tyr Gin Pro Thr Ile Asp Thr Ala
 245 250 255
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 atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg 816
 Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
 260 265 270
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 gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag 864
 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285
 25
 gct tcg gtg aca gtt cog tat tgg ggt gcc cgc aac gag ttg atc gaa 912
 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
 290 295 300
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 305 310 315 320
 35
 ctt cag tct cgacaa cgg tgc cga agc gta tcg acg act ggc tgc cgg 1008
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 325 330 335
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 aac gct cag cgg cgc tgc ggt tgc ggt ccc tgg tct gta gta cgg aca 1056
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 340 345 350
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 Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile
 355 360 365
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 cgg cgc ggc atc agt gtc aga aat tcg gtg tgc gct agc tgc acg cct 1152

01年12月04日(火) 15時10分 郵先: F E T F

発信:住友化学知的財産センター(株)

R:698 P. 02/14

Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro
370 375 380

cga tga 1158
5 Arg
385